

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Russell, John
Colpitts, Tracey
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6105.US.01
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/937-6100
(B) TELEFAX: 847/938-2623
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTGACCAT	GAAGGCTGTG	CTGCTTGCCC	TGTTGATGGC	AGGCTTGGCC	CTGCAGCCAG	60
GCACTGCCCT	GCTGTGCTAC	TCCTGCAAAG	CCCAGGTGAG	CAACGAGGAC	TGCCTGCAGG	120
TGGAGAACTG	CACCCAGCTG	GGGGAGCAGT	GCTGGACCGC	GCGCATCCGC	GCAGTTGGCC	180

TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAAGTGGCT GGATGACTCA CAGGACTACT	240
ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT	279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC	60
ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG	120
GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC	180
CTGACCGTCA TCAGCAAAGG CTGCAGC	207

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG	60
CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA	120
TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG	180
CAACGCCAGC GGGGCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC	240
ACTCGGCCTG CTGCTCTGGG GACCC	265

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCGGCCTGC TGCTCTGGGG ACCCGGCCAG CTATAGGCTC TGGGGGGGCC CGCTGCAGCC	60
CACACTGGGT GTGGTGCCCC AGGCCTCTGT GCCACTCCTC ACAGACCTGG CCCAGTGGGA	120
GCCTGTCTTG GTTCCTGAGG CACATCCTAA CGCAAGTCTG ACCATGTATG TCTGCACCCC	180
TGTNCCCCAC CCTGAC	196

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG	60
TATGTCTGCN CCCCTGTCCC CCACCCTGAC CCTCCCATGG CCCTCTCCAG GACTCCCACC	120
CGGCAGATCA GCTCTAGTGA CACAGATCCG CCTGCAGATG GCCCCTCCAA CCCTCTCTGC	180

TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT

233

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAGCATTC	TCCACCCTTA	ACCCTGTGCT	CAGGCACCTC	TTCCCCCAGG	AAGCCTTCCC	60
TGCCCCACCC	ATCTATGACT	TGAGCCAGGT	CTGGTCCGTG	GTGTCCCCCG	CACCCAGCAG	120
GGGACAGGCA	CTCAGGAGGG	CCCAGTAAAG	GCTGAGATGA	AGTGGACTGA	GTAGAACTGG	180
AGGACAAGAG	TCGACGTGAG	TTCCTGGGAG	TCTCCAGAGA	TGGGGCCTGG	AGGCCT	236

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGGGAGTC	TCCAGAGATG	GGGCCTGGAG	GCCTGGAGGA	ANGGNANCAG	GCCTCACATT	60
CGTGGGGCTC	CCTGAATGGC	AGCCTGAGCA	CAGCGTAGGC	CCTTAATAAA	CACCTGTTGG	120
AT						122

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGTGACCAT	GAAGGCTGTG	CTGCTTGCCC	TGTTGATGGC	AGGCTTGGCC	CTGCAGCCAG	60
GCACTGCCCT	GCTGTGCTAC	TCCTGCAAAG	CCCAGGTGAG	CAACGAGGAC	TGCCTGCAGG	120
TGGAGAAGTG	CACCCAGCTG	GGGGAGCAGT	GCTGGACCGC	GCGCATCCGC	GCAGTTGGCC	180
TCCTGACCGT	CATCAGCAAA	GGCTGCAGCT	TGAACTGCGT	GGATGACTCA	CAGGACTACT	240
ACGTGGGCAA	GAAGAACATC	ACGTGCTGTG	ACACCGACTT	GTGCAACGCC	AGCGGGGCCC	300
ATGCCCTGCA	GCCGGCTGCC	GCCATCCTTG	CGCTGCTCCC	TGCACTCGGC	CTGCTGCTCT	360
GGGGACCCGG	CCAGCTATAG	GCTCTGGGGG	GCCCCGCTGC	AGCCCACACT	GGGTGTGGTG	420
CCCCAGGCCT	CTGTGCCACT	CCTCACAGAC	CTGGCCCAGT	GGGAGCCTGT	CCTGGTTCCT	480
GAGGCACATC	CTAACGCAAG	TCTGACCATG	TATGTCTGCA	CCCCTGTCCC	CCACCCTGAC	540
CCTCCCATGG	CCCTCTCCAG	GACTCCCACC	CGGCAGATCA	GCTCTAGTGA	CACAGATCCG	600
CCTGCAGATG	GCCCCTCCAA	CCCTCTCTGC	TGCTGTTTCC	ATGGCCCAGC	ATTCTCCACC	660
CTTAACCCTG	TGCTCAGGCA	CCTCTTCCCC	CAGGAAGCCT	TCCCTGCCCA	CCCCATCTAT	720
GACTTGAGCC	AGGTCTGGTC	CGTGGTGTCC	CCCGCACCCA	GCAGGGGACA	GGCACTCAGG	780
AGGGCCCAGT	AAAGGCTGAG	ATGAAGTGGA	CTGAGTAGAA	CTGGAGGACA	AGAGTCGACG	840
TGAGTTCCTG	GGAGTCTCCA	GAGATGGGGC	CTGGAGGCCT	GGAGGAANGG	NANCAGGCCT	900
CACATTTCGTG	GGGCTCCCTG	AATGGCAGCC	TGAGCACAGC	GTAGGCCCTT	AATAAACACC	960
TGTTGGAT						968

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC
CGGGAATT

60
68

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG
GAATTCCG

60
68

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Lys	Ala	Val	Leu	Leu	Ala	Leu	Leu	Met	Ala	Gly	Leu	Ala	Leu	Gln
1				5					10					15	
Pro	Gly	Thr	Ala	Leu	Leu	Cys	Tyr	Ser	Cys	Lys	Ala	Gln	Val	Ser	Asn
			20					25					30		
Glu	Asp	Cys	Leu	Gln	Val	Glu	Asn	Cys	Thr	Gln	Leu	Gly	Glu	Gln	Cys
		35				40						45			
Trp	Thr	Ala	Arg	Ile	Arg	Ala	Val	Gly	Leu	Leu	Thr	Val	Ile	Ser	Lys
		50				55					60				
Gly	Cys	Ser	Leu	Asn	Cys	Val	Asp	Asp	Ser	Gln	Asp	Tyr	Tyr	Val	Gly
65				70					75					80	
Lys	Lys	Asn	Ile	Thr	Cys	Cys	Asp	Thr	Asp	Leu	Cys	Asn	Ala	Ser	Gly
			85					90						95	
Ala	His	Ala	Leu	Gln	Pro	Ala	Ala	Ala	Ile	Leu	Ala	Leu	Leu	Pro	Ala
			100					105					110		
Leu	Gly	Leu	Leu	Leu	Trp	Gly	Pro	Gly	Gln	Leu					
		115				120									

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr	Ala	Leu	Leu	Cys	Tyr	Ser	Cys	Lys	Ala	Gln	Val	Ser	Asn	Glu	Asp
1				5				10						15	

Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr
 20 25 30
 Ala Arg

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser
 1 5 10 15
 Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn
 20 25 30
 Ile Thr Cys Cys Asp Thr Asp Leu Cys
 35 40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr
 1 5 10 15
 Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly Ala His Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala Leu Gly Leu
 1 5 10 15
 Leu Trp Gly Pro Gly Gln Leu
 20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5